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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=11; day=24; hr=10; min=49; sec=29; ms=158;]

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Reviewer Comments:

<160> 9

<170> KopatentIn 1.71

The number provided for numeric identifier <160> must match the total number of sequences in the file. There are 11 sequences in this sequence listing but, 9 is given as the total in numeric identifier <160>, "<160> 9." Please make all necessary changes.

<210> 5

<211> 68

<212> PRT

<213> Artificial Sequence

<400> 5

For all sequences using "Artificial sequence", for numeric identifier <213>, a mandatory feature is required to explain the source of the genetic material. The feature consists of <220>, which remains blank, and <223>, which states the source of the genetic material. To explain the source, if the sequence is put together from several organisms, please list those organisms. If the sequence is made in the laboratory, please indicate that the sequence is synthesized. These errors appear in other sequences in the sequence listing. Please make all necessary changes.

Application No: 10593413 Version No: 1.0

Input Set:**Output Set:**

Started: 2008-10-28 16:16:48.335
Finished: 2008-10-28 16:16:52.980
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 645 ms
Total Warnings: 9
Total Errors: 34
No. of SeqIDs Defined: 9
Actual SeqID Count: 11

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (5)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (8)
E 300	Invalid codon found Gly SEQID (8) POS: 337
E 300	Invalid codon found Gly SEQID (8) POS: 340
E 300	Invalid codon found Ser SEQID (8) POS: 343
E 300	Invalid codon found Ser SEQID (8) POS: 346
E 300	Invalid codon found Ser SEQID (8) POS: 349
E 300	Invalid codon found Gly SEQID (8) POS: 352
E 300	Invalid codon found Thr SEQID (8) POS: 355
E 300	Invalid codon found Val SEQID (8) POS: 358

Input Set:

Output Set:

Started: 2008-10-28 16:16:48.335

Finished: 2008-10-28 16:16:52.980

Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 645 ms

Total Warnings: 9

Total Errors: 34

No. of SeqIDs Defined: 9

Actual SeqID Count: 11

Error code	Error Description
E 300	Invalid codon found Asn SEQID (8) POS: 361
E 300	Invalid codon found Pro SEQID (8) POS: 364
E 300	Invalid codon found Val SEQID (8) POS: 367
E 300	Invalid codon found Pro SEQID (8) POS: 370
E 300	Invalid codon found Thr SEQID (8) POS: 373
E 300	Invalid codon found Thr SEQID (8) POS: 376
E 300	Invalid codon found Ala SEQID (8) POS: 379
E 300	Invalid codon found Ser SEQID (8) POS: 382
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (9)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
E 323	Invalid/missing amino acid numbering SEQID (10) POS (337)
E 323	Invalid/missing amino acid numbering SEQID (10) POS (343)
E 323	Invalid/missing amino acid numbering SEQID (10) POS (352)
E 323	Invalid/missing amino acid numbering SEQID (10) POS (358)
E 323	Invalid/missing amino acid numbering SEQID (10) POS (367)
E 323	Invalid/missing amino acid numbering SEQID (10) POS (373)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (11)

Input Set:

Output Set:

Started: 2008-10-28 16:16:48.335
Finished: 2008-10-28 16:16:52.980
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 645 ms
Total Warnings: 9
Total Errors: 34
No. of SeqIDs Defined: 9
Actual SeqID Count: 11

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 252	Calc# of Seq. differs from actual; 9 seqIds defined; count=11

Sequence Listing

<110> SJ BIOMED INC.

<120> Anti-obese immunogenic hybrid polypeptides and anti-obese vaccine composition comprising the same

<160> 9

<170> KopatentIn 1.71

<210> 1

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> mimetic peptide for apolipoprotein B-100 epitope

<400> 1

Arg	Asn	Val	Pro	Pro	Ile	Phe	Asn	Asp	Val	Tyr	Trp	Ile	Ala	Phe
1				5					10					15

<210> 2

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> mimetic peptide for apolipoprotein B-100 epitope

<400> 2

Arg	Phe	Arg	Gly	Leu	Ile	Ser	Leu	Ser	Gln	Val	Tyr	Leu	Asp	Pro
1				5					10					15

<210> 3

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> mimetic peptide for apolipoprotein B-100 epitope

<400> 3

Ser	Val	Cys	Gly	Cys	Pro	Val	Gly	His	His	Asp	Val	Val	Gly	Leu
1				5					10					15

<210> 4

<211> 204

<212> DNA

<213> Artificial Sequence

<120> Anti-obese immunogenic hybrid polypeptides and anti-obese vaccine composition comprising the same

<220>
<223> DNA sequence for terameric mimetic peptide

<220>
<221> CDS
<222> (1)..(204)

<400> 4
gtc gac cgt aat gtt cct cct atc ttc aat gat gtt tat tgg att gca 48
Val Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala
1 5 10 15

ttc ctc gac cgt aat gtt cct cct atc ttc aat gat gtt tat tgg att 96
Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile
20 25 30

gca ttc ctc gac cgt aat gtt cct cct atc ttc aat gat gtt tat tgg 144
Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp
35 40 45

att gca ttc ctc gac cgt aat gtt cct cct atc ttc aat gat gtt tat 192
Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr
50 55 60

tgg att gca ttc 204
Trp Ile Ala Phe
65

<210> 5
<211> 68

<212> PRT
<213> Artificial Sequence
<400> 5
Val Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala
1 5 10 15

Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile
20 25 30

Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp
35 40 45

Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr
50 55 60

Trp Ile Ala Phe
65

<210> 6

<211>180

<212>DNA

<213>Hepatitis B virus

<220>

<221>CDS

<222>(1)..(177)

<223>Hepatitis B virus preS2

<220>

<221>terminator

<222>(178)..(180)

<400>6

atg cag tgg aac tcc acc aca ttc cac caa gct ctg cta gat ccc aga48

Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu Asp Pro Arg

15105

gtg agg ggc cta tat ttt cct gct ggt ggc tcc agt tcc gga aca gta96

Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val

202530

aac cct gtt ccg act act gcc tca ccc ata tcg tca atc ttc tcg agg144

Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Ser Ile Phe Ser Arg

354045

act ggg gac cct gca ccg aac ctc gag cgg tca180

Thr Gly Asp Pro Ala Pro Asn Leu Glu Arg Ser

5055

<210>7

<211>59

<212>PRT

<213>Hepatitis B virus

<400>7

Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu Asp Pro Arg

15105

Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val

202530

Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Ser Ile Phe Ser Arg

354045

Thr Gly Asp Pro Ala Pro Asn Leu Glu Arg Ser

5055

<210>8

<211>444

<212>DNA

<213>Artificial Sequence

<220>

<223> DNA sequence for hybride polypeptide

<220>

<221> CDS

<222> (1)..(441)

<220>

<221> terminator

<222> (441)..(444)

<400> 8

atg	aga	gga	tcg	cat	cac	cat	cac	cat	cac	gga	tcc	gat	gat	gat	gac	48
Met	Arg	Gly	Ser	His	His	His	His	His	His	Gly	Ser	Asp	Asp	Asp	Asp	
1			5					10				15				

aag	atc	gtc	gac	cgt	aat	gtt	cct	cct	atc	ttc	aat	gat	gtt	tat	tgg	96
Lys	Ile	Val	Asp	Arg	Asn	Val	Pro	Pro	Ile	Phe	Asn	Asp	Val	Tyr	Trp	
		20					25					30				

att	gca	ttc	ctc	gac	cgt	aat	gtt	cct	cct	atc	ttc	aat	gat	gtt	tat	144
Ile	Ala	Phe	Leu	Asp	Arg	Asn	Val	Pro	Pro	Ile	Phe	Asn	Asp	Val	Tyr	
	35						40					45				

tgg	att	gca	ttc	ctc	gac	cgt	aat	gtt	cct	cct	atc	ttc	aat	gat	gtt	192
Trp	Ile	Ala	Phe	Leu	Asp	Arg	Asn	Val	Pro	Pro	Ile	Phe	Asn	Asp	Val	
	50					55					60					

tat	tgg	att	gca	ttc	ctc	gac	cgt	aat	gtt	cct	cct	atc	ttc	aat	gat	240
Tyr	Trp	Ile	Ala	Phe	Leu	Asp	Arg	Asn	Val	Pro	Pro	Ile	Phe	Asn	Asp	
	65				70					75				80		

gtt	tat	tgg	att	gca	ttc	ctc	gac	atg	cag	tgg	aac	tcc	acc	aca	ttc	288
Val	Tyr	Trp	Ile	Ala	Phe	Leu	Asp	Met	Gln	Trp	Asn	Ser	Thr	Thr	Phe	
				85					90					95		

cac	caa	gct	ctg	cta	gat	ccc	aga	gtg	agg	ggc	cta	tat	ttt	cct	gct	336
His	Gln	Ala	Leu	Leu	Asp	Pro	Arg	Val	Arg	Gly	Leu	Tyr	Phe	Pro	Ala	
		100					105						110			

ggc	ggc	tcc	agt	tcc	gga	aca	gta	aac	cct	gtt	ccg	act	act	gcc	tca	384
Gly	Gly	Ser	Ser	Ser	Gly	Thr	Val	Asn	Pro	Val	Pro	Thr	Thr	Ala	Ser	
					115				120					125		

ccc	ata	tcg	tca	atc	ttc	tcg	agg	act	ggg	gac	cct	gca	ccg	aac	ctc	432
Pro	Ile	Ser	Ser	Ile	Phe	Ser	Arg	Thr	Gly	Asp	Pro	Ala	Pro	Asn	Leu	
	130					135				140						

gag	cgg	tca	taa													444
Glu	Arg	Ser														
145																

<210> 9

<211> 147

<212> PRT
<213> Artificial Sequence

<400> 9
Met Arg Gly Ser His His His His His His Gly Ser Asp Asp Asp Asp
1 5 10 15
Lys Ile Val Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp
20 25 30
Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr
35 40 45
Trp Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val
50 55 60
Tyr Trp Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp
65 70 75 80
Val Tyr Trp Ile Ala Phe Leu Asp Met Gln Trp Asn Ser Thr Thr Phe
85 90 95
His Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala
100 105 110
Gly Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser
115 120 125
Pro Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Leu
130 135 140
Glu Arg Ser
145

<210> 10
<211> 432
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA sequence for PTB14

<220>
<221> CDS
<222> (1)..(429)

<400> 10
atg aga gga tcg cat cac cat cac cat cac gga tcc gat gat gat gac 48
Met Arg Gly Ser His His His His His His Gly Ser Asp Asp Asp Asp
1 5 10 15
aag atc gtc gac atg cag tgg aac tcc acc aca ttc cac caa gct ctg 96
Lys Ile Val Asp Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu

20	25	30	
cta gat ccc aga gtg agg ggc cta tat ttt cct gct ggt ggc tcc agt			144
Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser			
35	40	45	
tcc gga aca gta aac cct gtt ccg act act gcc tca ccc ata tcg tca			192
Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Ser			
50	55	60	
atc ttc tcg aag act ggg gac cct gca ccg aac ctc gac cgt aat gtt			240
Ile Phe Ser Lys Thr Gly Asp Pro Ala Pro Asn Leu Asp Arg Asn Val			
65	70	75	80
cct cct atc ttc aat gat gtt tat tgg att gca ttc ctc gac cgt aat			288
Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp Arg Asn			
85	90	95	
gtt cct cct atc ttc aat gat gtt tat tgg att gca ttc ctc gac cgt			336
Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp Arg			
100	105	110	
aat gtt cct cct atc ttc aat gat gtt tat tgg att gca ttc ctc gac			384
Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp			
115	120	125	
cgt aat gtt cct cct atc ttc aat gat gtt tat tgg att gca ttc			430
Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe			
130	135	140	
aa			432

<210> 11
 <211> 143
 <212> PRT
 <213> Artificial Sequence

<400> 11
 Met Arg Gly Ser His His His His His His Gly Ser Asp Asp Asp Asp
 1 5 10 15
 Lys Ile Val Asp Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu
 20 25 30
 Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser
 35 40 45
 Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Ser
 50 55 60
 Ile Phe Ser Lys Thr Gly Asp Pro Ala Pro Asn Leu Asp Arg Asn Val
 65 70 75 80
 Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp Arg Asn

85

90

95

Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp Arg
100 105 110

Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp
115 120 125

Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe
130 135 140